

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/828, 559

Source: IFW

Date Processed by STIC: 12-22-04

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 12/22/2004

PATENT APPLICATION: US/10/828,559

TIME: 15:34:24

Input Set : A:\0334.210US-seqlist.txt

Output Set: N:\CRF4\12222004\J828559.raw

4 <110> APPLICANT: Punnonen, Juha
 5 Apt, Doris
 6 Neighbors, Margaret
 7 Leong, Steven R.
 9 <120> TITLE OF INVENTION: NOVEL TUMOR-ASSOCIATED ANTIGENS
 12 <130> FILE REFERENCE: 0334.210US
 14 <140> CURRENT APPLICATION NUMBER: US 10/828,559
 15 <141> CURRENT FILING DATE: 2004-04-19
 17 <150> PRIOR APPLICATION NUMBER: US 60/464,780
 18 <151> PRIOR FILING DATE: 2003-04-22
 20 <160> NUMBER OF SEQ ID NOS: 95
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 185
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: TAG-25 fragment comprising extra-cellular domain
 31 (ECD)
 33 <400> SEQUENCE: 1
 34 Arg Ile Lys Pro Glu Gly Ala Leu Gln Asn Asp Gly Leu Tyr Asp
 35 1 5 10 15
 36 Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
 37 20 25 30
 38 Thr Ala Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
 39 35 40 45
 40 Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
 41 50 55 60
 42 Ile Ile Glu Leu Lys His Lys Glu Arg Glu Ser Pro Tyr Asp Ser Lys
 43 65 70 75 80
 44 Ser Leu His Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
 45 85 90 95
 46 Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
 47 100 105 110
 48 Ile Asp Leu Met Gln Asn Ser Ser Gln Lys Thr Gln Asp Asp Val Asp
 49 115 120 125
 50 Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
 51 130 135 140
 52 Leu Phe His Ser Lys Lys Met Asp Leu Arg Val Asn Gly Glu Leu Leu
 53 145 150 155 160
 54 Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
 55 165 170 175
 56 Pro Glu Phe Ser Met Gln Gly Leu Lys

(ps.6)

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57          180          185
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 57
62 <212> TYPE: PRT
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: TAg-25 fragment comprising propeptide (PP)
68 <400> SEQUENCE: 2
69 Gln Glu Glu Cys Val Cys Glu Asn Tyr Lys Leu Ala Val Asn Cys Phe
70 1          5          10          15
71 Val Asn Asn Asn Arg Glu Cys Gln Cys Thr Ser Val Gly Ala Gln Asn
72          20          25          30
73 Thr Val Ile Cys Ser Lys Leu Ala Ala Lys Cys Leu Val Met Lys Ala
74          35          40          45
75 Glu Met Asn Gly Ser Lys Leu Gly Arg
76          50          55
79 <210> SEQ ID NO: 3
80 <211> LENGTH: 23
81 <212> TYPE: PRT
82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: TAg-25 fragment comprising signal peptide (SP)
87 <400> SEQUENCE: 3
88 Met Ala Pro Pro Gln Ala Leu Ala Leu Gly Leu Leu Leu Ala Ala Ala
89 1          5          10          15
90 Thr Ala Thr Phe Ala Ala Ala
91          20
94 <210> SEQ ID NO: 4
95 <211> LENGTH: 265
96 <212> TYPE: PRT
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: TAg-25 polypeptide (which comprises signal
101 peptide+propeptide+ ECD)
103 <400> SEQUENCE: 4
104 Met Ala Pro Pro Gln Ala Leu Ala Leu Gly Leu Leu Leu Ala Ala Ala
105 1          5          10          15
106 Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
107          20          25          30
108 Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Glu Cys Gln Cys
109          35          40          45
110 Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
111          50          55          60
112 Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
113 65          70          75          80
114 Arg Ile Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
115          85          90          95
116 Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
117          100          105          110

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118 Thr Ala Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
119      115      120      125
120 Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
121      130      135      140
122 Ile Ile Glu Leu Lys His Lys Glu Arg Glu Ser Pro Tyr Asp Ser Lys
123 145      150      155      160
124 Ser Leu His Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
125      165      170      175
126 Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
127      180      185      190
128 Ile Asp Leu Met Gln Asn Ser Ser Gln Lys Thr Gln Asp Asp Val Asp
129      195      200      205
130 Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
131      210      215      220
132 Leu Phe His Ser Lys Lys Met Asp Leu Arg Val Asn Gly Glu Leu Leu
133 225      230      235      240
134 Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
135      245      250      255
136 Pro Glu Phe Ser Met Gln Gly Leu Lys
137      260      265
140 <210> SEQ ID NO: 5
141 <211> LENGTH: 242
142 <212> TYPE: PRT
143 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: TAg-25 fragment comprising propeptide+ ECD
146 <400> SEQUENCE: 5
149 Gln Glu Glu Cys Val Cys Glu Asn Tyr Lys Leu Ala Val Asn Cys Phe
150 1      5      10      15
151 Val Asn Asn Asn Arg Glu Cys Gln Cys Thr Ser Val Gly Ala Gln Asn
152      20      25      30
153 Thr Val Ile Cys Ser Lys Leu Ala Ala Lys Cys Leu Val Met Lys Ala
154      35      40      45
155 Glu Met Asn Gly Ser Lys Leu Gly Arg Arg Ile Lys Pro Glu Gly Ala
156      50      55      60
157 Leu Gln Asn Asn Asp Gly Leu Tyr Asp Pro Asp Cys Asp Glu Ser Gly
158 65      70      75      80
159 Leu Phe Lys Ala Lys Gln Cys Asn Gly Thr Ala Thr Cys Trp Cys Val
160      85      90      95
161 Asn Thr Ala Gly Val Arg Arg Thr Asp Lys Asp Thr Glu Ile Thr Cys
162      100      105      110
163 Ser Glu Arg Val Arg Thr Tyr Trp Ile Ile Ile Glu Leu Lys His Lys
164      115      120      125
165 Glu Arg Glu Ser Pro Tyr Asp Ser Lys Ser Leu His Thr Ala Leu Gln
166      130      135      140
167 Lys Glu Ile Thr Thr Arg Tyr Gln Leu Asp Pro Lys Phe Ile Thr Ser
168 145      150      155      160
169 Ile Leu Tyr Glu Asn Asn Val Ile Thr Ile Asp Leu Met Gln Asn Ser
170      165      170      175

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```

171 Ser Gln Lys Thr Gln Asp Asp Val Asp Ile Ala Asp Val Ala Tyr Tyr
172      180      185      190
173 Phe Glu Lys Asp Val Lys Gly Glu Ser Leu Phe His Ser Lys Lys Met
174      195      200      205
175 Asp Leu Arg Val Asn Gly Glu Leu Leu Asp Leu Asp Pro Gly Gln Thr
176      210      215      220
177 Leu Ile Tyr Tyr Val Asp Glu Lys Ala Pro Glu Phe Ser Met Gln Gly
178 225      230      235      240
179 Leu Lys
183 <210> SEQ ID NO: 6
184 <211> LENGTH: 314
185 <212> TYPE: PRT
186 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: TAG-25 full-length/membrane-bound form, which
190     comprises N- to C-terminus signal
191     peptide+propeptide+ECD+TMD+CD
193 <400> SEQUENCE: 6
194 Met Ala Pro Pro Gln Ala Leu Ala Leu Gly Leu Leu Leu Ala Ala Ala
195 1      5      10      15
196 Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
197      20      25      30
198 Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Glu Cys Gln Cys
199      35      40      45
200 Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
201      50      55      60
202 Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
203 65      70      75      80
204 Arg Ile Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
205      85      90      95
206 Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
207      100     105     110
208 Thr Ala Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
209      115     120     125
210 Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
211      130     135     140
212 Ile Ile Glu Leu Lys His Lys Glu Arg Glu Ser Pro Tyr Asp Ser Lys
213 145     150     155     160
214 Ser Leu His Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
215      165     170     175
216 Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
217      180     185     190
218 Ile Asp Leu Met Gln Asn Ser Ser Gln Lys Thr Gln Asp Asp Val Asp
219      195     200     205
220 Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
221      210     215     220
222 Leu Phe His Ser Lys Lys Met Asp Leu Arg Val Asn Gly Glu Leu Leu
223 225     230     235     240
224 Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala

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```

225          245          250          255
226 Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
227          260          265          270
228 Val Val Val Val Met Ala Val Val Ala Gly Ile Val Val Leu Val Ile
229          275          280          285
230 Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
231          290          295          300
232 Met Gly Glu Met His Arg Glu Leu Asn Ala
233 305          310
236 <210> SEQ ID NO: 7
237 <211> LENGTH: 234
238 <212> TYPE: PRT
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Mature Tag-25 polypeptide, which comprises N- to
243 C-terminus ECD+TMD+CD
245 <220> FEATURE:
246 <221> NAME/KEY: DOMAIN
247 <222> LOCATION: (186)...(208)
248 <223> OTHER INFORMATION: Transmembrane domain (TMD)
250 <400> SEQUENCE: 7
251 Arg Ile Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
252 1          5          10          15
253 Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
254          20          25          30
255 Thr Ala Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
256          35          40          45
257 Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
258          50          55          60
259 Ile Ile Glu Leu Lys His Lys Glu Arg Glu Ser Pro Tyr Asp Ser Lys
260 65          70          75          80
261 Ser Leu His Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
262          85          90          95
263 Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
264          100          105          110
265 Ile Asp Leu Met Gln Asn Ser Ser Gln Lys Thr Gln Asp Asp Val Asp
266          115          120          125
267 Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
268          130          135          140
269 Leu Phe His Ser Lys Lys Met Asp Leu Arg Val Asn Gly Glu Leu Leu
270 145          150          155          160
271 Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
272          165          170          175
273 Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
274          180          185          190
275 Val Val Val Val Met Ala Val Val Ala Gly Ile Val Val Leu Val Ile
276          195          200          205
277 Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
278          210          215          220

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/22/2004
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:81; Xaa Pos. 2,3,7,12,13,14,16,17,19,20,21,22,28,30,41,47,48,51
Seq#:82; Xaa Pos. 2,3,14,16,17,19,20,21,22,28,30,47,48,51
Seq#:83; Xaa Pos. 3,5,6,9,15,16,20
Seq#:84; Xaa Pos. 2,4,5,6,7,8,9,10,11,13,14,15,16,17,18,19,21,23,24,25,26
Seq#:84; Xaa Pos. 27,28,29,30,31,32
Seq#:85; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:85; Xaa Pos. 24,25,26,27,28,29,30,31,32,33,35,36,37,38,39,40,41,42,43
Seq#:85; Xaa Pos. 44,46,47,48,49,50,52,54,55,56,57,58,59,60,61,62,63,64,65
Seq#:85; Xaa Pos. 66,67,68,69
Seq#:86; Xaa Pos. 11,13,14,15,16,17,18,19,21,23,24,25,26,27,28,29,30,31,32
Seq#:87; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,17,18,19,20,21,22,23,42,43
Seq#:87; Xaa Pos. 44,46,47,48,58,59,60,61,62,63,64,65,66,67,68,69
Seq#:88; Xaa Pos. 2,4,5,6,7,8,9,10,11,13,14,15,16,17,18,19,21,23,24,25,26
Seq#:88; Xaa Pos. 27,28,29,30,31,32,34,35,36,37,38,39,41,42,43,44,45,46,47
Seq#:88; Xaa Pos. 48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66
Seq#:88; Xaa Pos. 67,68,69,70,71,72,74,75,76,77,78,79,80,81,82,83,85,86,87
Seq#:88; Xaa Pos. 88,89,91,93,94,95,96,97,98,99,100,101,102,103,104,105,106
Seq#:88; Xaa Pos. 107,108
Seq#:89; Xaa Pos. 11,13,14,15,16,17,18,19,21,23,24,25,26,27,28,29,30,31,32
Seq#:89; Xaa Pos. 34,35,36,37,38,39,41,42,43,44,45,46,47,48,49,50,51,52,53
Seq#:89; Xaa Pos. 56,57,58,59,60,61,62,81,82,83,85,86,87,97,98,99,100,101
Seq#:89; Xaa Pos. 102,103,104,105,106,107,108
Seq#:90; Xaa Pos. 2,3,4,5,6,7,8,27,28,29,31,32,33,43,44,45,46,47,48,49,50
Seq#:90; Xaa Pos. 51,52,53,54
Seq#:91; Xaa Pos. 2,6,7,8,9,10,11,13,14,15,16,17,18,19,20,25,26,27,28,32,34
Seq#:91; Xaa Pos. 38,40,41,43,44,47,48,49,50,51,52,58,59,61,62,63,64,65,66
Seq#:91; Xaa Pos. 68,69,70

VERIFICATION SUMMARY

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L:1902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0
M:341 Repeated in SeqNo=81
L:1927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0
M:341 Repeated in SeqNo=82
L:1951 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
M:341 Repeated in SeqNo=83
L:1971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:0
M:341 Repeated in SeqNo=84
L:1993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:0
M:341 Repeated in SeqNo=85
L:2019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
M:341 Repeated in SeqNo=86
L:2047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0
M:341 Repeated in SeqNo=87
L:2073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88 after pos.:0
M:341 Repeated in SeqNo=88
L:2108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:89 after pos.:0
M:341 Repeated in SeqNo=89
L:2143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90 after pos.:0
M:341 Repeated in SeqNo=90
L:2168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:0
M:341 Repeated in SeqNo=91